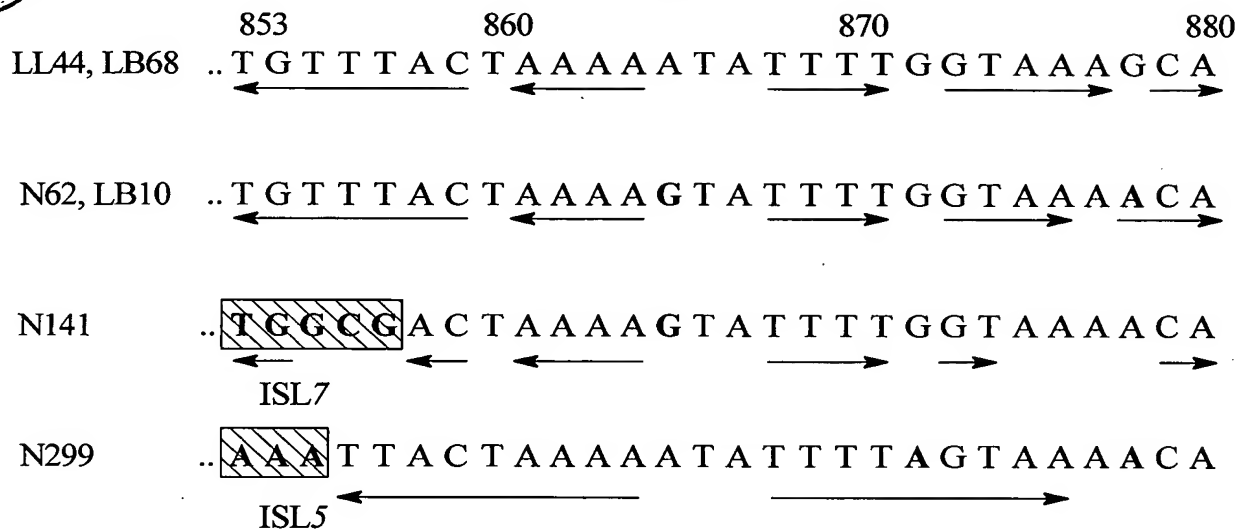


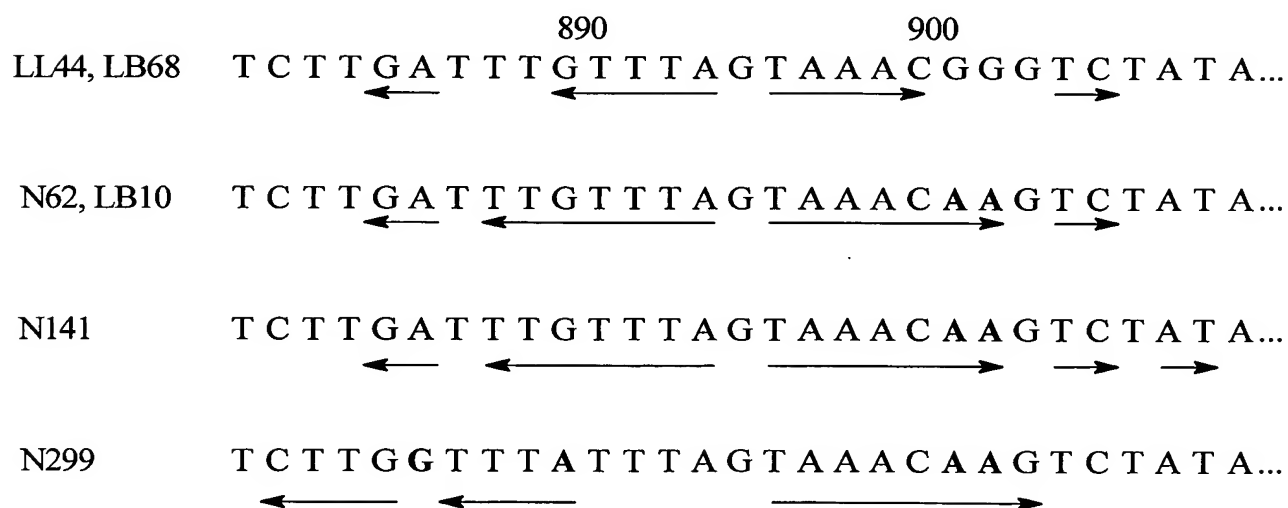
FIG. 1



O1



O2



LL44, LB68

lacA

O1

O2

lacS

lacSZR

860 880 900 940

CRE 920 *****

TTTTGTACTAAAAATATTTGGTAAAGCATCTTGATTGTTAGTAAACGGGTCTATACCTGTAAAGCGTAAACAAAGTTAGAACACCTAAAGGAGAAAATCATGAA
 AAAACAAATGATTTTATAAAACCATTTGCTAGAACTAAACAAATCAATTTGCCAGATATGACATTCGCATTTGTTCATCTGTGGATTTCCTCTTTTAGTACIT

O1

O2

start

lacS

[illegible]

FIG. 4

1 GAATTTTGTCTGGATGCTCAGGAAGCCCGCCAGCTCAAGCTGGTGATTGAGCCACTTTTT
stop lacZ
61 ACTGAA[TAA]TGCTACAATTGACTTAACAGCATATAAATTTTAGTAAAAGCGAGTGAAGAAG
RBS
121 [ATG]GCAACGATCAGAGAAGTGGCCAAGGCAGCCGGCGTGTGCGCCAGCGACGGTTTCCCGG
1 M A T I R E V A K A A G V S P A T V S R
helix turn helix
181 GTCTTGAACATATGACCAGACCCTGTCGGTCAATGAGGCAACGCGGCAGAAAGATATTCAAA
21 V L N Y D Q T L S V N E A T R Q K I F K
241 ACTGCTGAAGCCATGCACTACCATAAGAGCCGGAAGACCAGAAAGAGCAAGCAAAAAGCGC
41 T A E A M H Y H K S R K T R K S K Q K R
301 CTGGCGATCTGCCTGTGGTGTGACCAAGACCAGGAGATCAAGGACCTCTATTACTATTCA
61 L A I C L W C D Q D Q E I K D L Y Y Y S
361 ATCAGAACCGCGCGCAAGCAGAGGCCAAGAAGCAGGGACTTGAAAGCCAGGTCATTTAT
81 I R T S A Q A E A K K Q G L E S Q V I Y
421 CCGGCTGATCCTTTGCCCGATCCAGCTGCTTTAAGCGGGATTATCATGATTGGCTACCAG
101 P A D P L P D P A A L S G I I M I G Y Q
481 CAGTATTCGCCAGACCGCTTGAATGAAGTCAAAAAGTCTGGCCTGCCCTGGTCTTTGTC
121 Q Y S P D R L N E V K K S G L P L V F V
541 GATACTGACACCTTAAAATTGGGTTACTGCTCAGTTGTGGCTGACTTTGGCCAGGCCATG
141 D T D T L K L G Y C S V V A D F G Q A M
601 CAGGAGGCGCTAGAGGTCTTCTGGGGGCAGGGCAGGGAGCGGATCGCCCTTTTGGATGGT
161 Q E A L E V F W G Q G R E R I A L L D G
661 GATTTGGACAGTAATTTTGATAAAAACAACCTTGGTCGACTTCCGCTTCCGCGATTATAAG
181 D L D S N F D K N N L V D F R F R D Y K
▼
721 AAGAGCCTCGCGGCCCGCGGCCAGTACGACCCGGACTTAGTCTATGTTGGAAACTTCACT
201 K S L A A R G Q Y D P D L V Y V G N F T
781 CCGCAATCTGGCTATGAAGCCATTAAAGAAGCTCTTAAGTCCGGCTCCTTCCCGAAAGCC
221 P Q S G Y E A I K E A L K S G S F P K A
841 TTGATTGCGGCTAATGACGCCATGGCTATTGGAGCATTGAAGGCCTTTAAAGAAGCTGGA
241 L I A A N D A M A I G A L K A F K E A G
901 ATTAAGTCCAGAGGACGTCAGTCTGATTCTTTTAATGACACAACGGCAGCAGAATTT
261 I K V P E D V S L I S F N D T T A A E F
961 GCCAACCCAGCCTTGACTAGCGTACATGTAGAGAC[CAG]CAGATGGGCCGAGCCAGCGTC
281 A N P A L T S V H V E T Q Q M G R A S V
1021 AAGGTCATGAAAGACCTGCTGGATGATGATGAAGCCGGCACTTACAAGGTCACCTTCCCA
301 K V M K D L L D D D E A G T Y K V T F P
1081 ACAAACTCGTTTACCGGGAATCTTGCCCAAAAGCATAAGGGCATAGAGCATAATAACAG
321 T K L V Y R E S C P K A *
1141 CAAAGAAATAGCTTGGAGATTGATTTTCTCCAAGCTATTTTTCGTATATA[TTA]TGGCTGC
stop asnA
1201 ATTCTGTTGATCATTCTTGGGAATGGGACAGCTTCACGAACGTGGTCCAGCTTGCAGATC
1261 CAGGCAATGACCCGTTCAAAG

FIG. 5

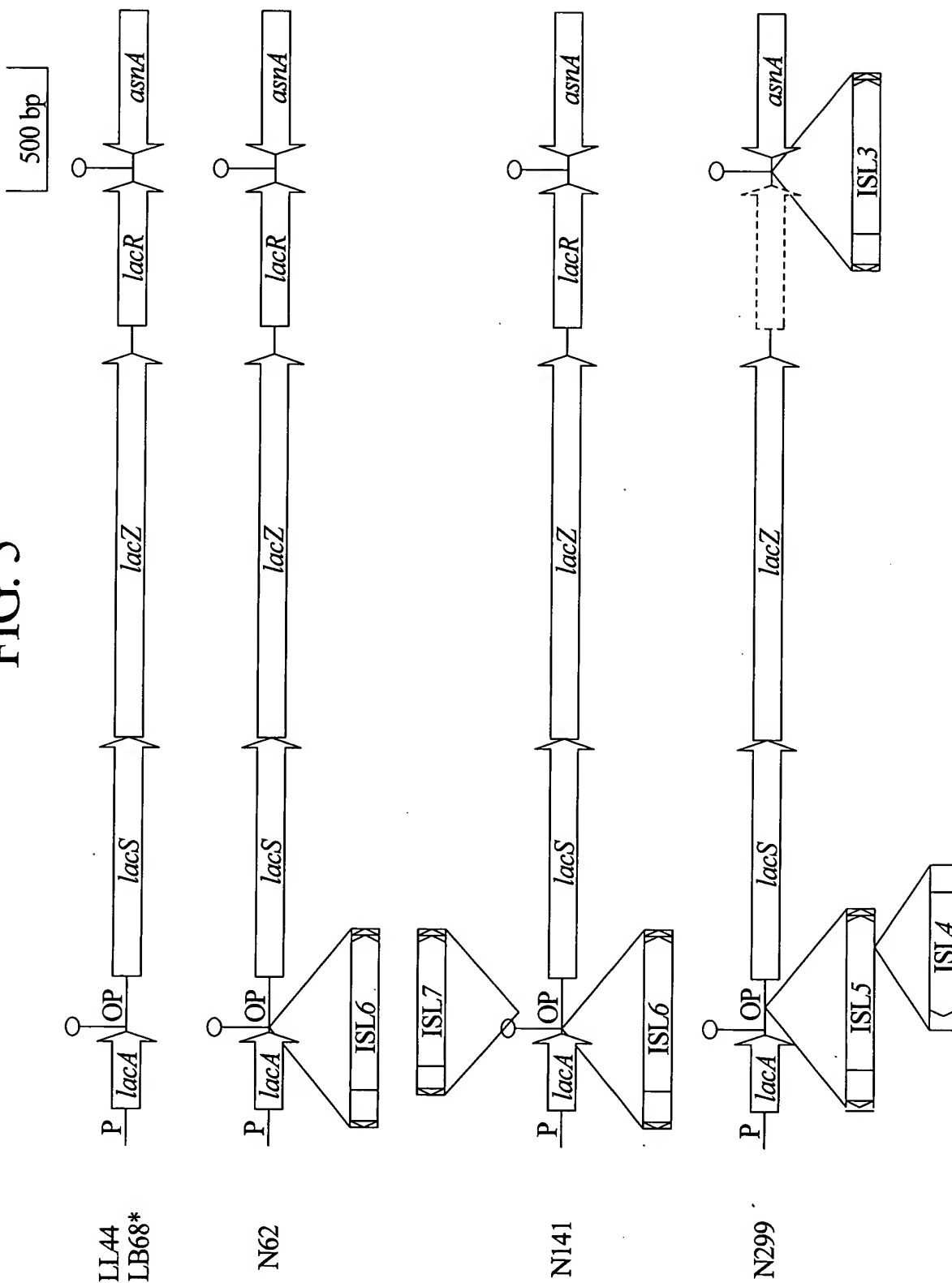


FIG. 6

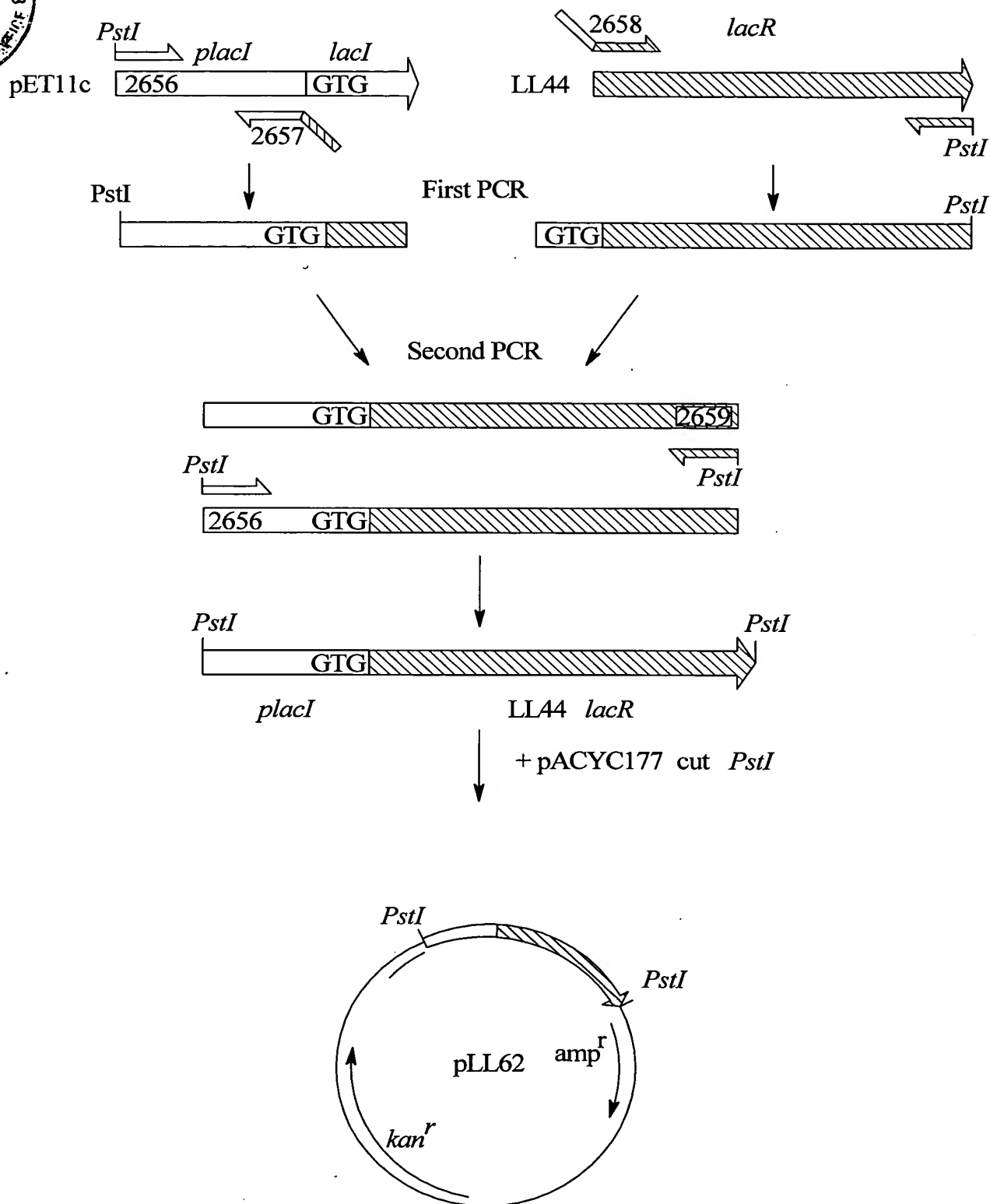
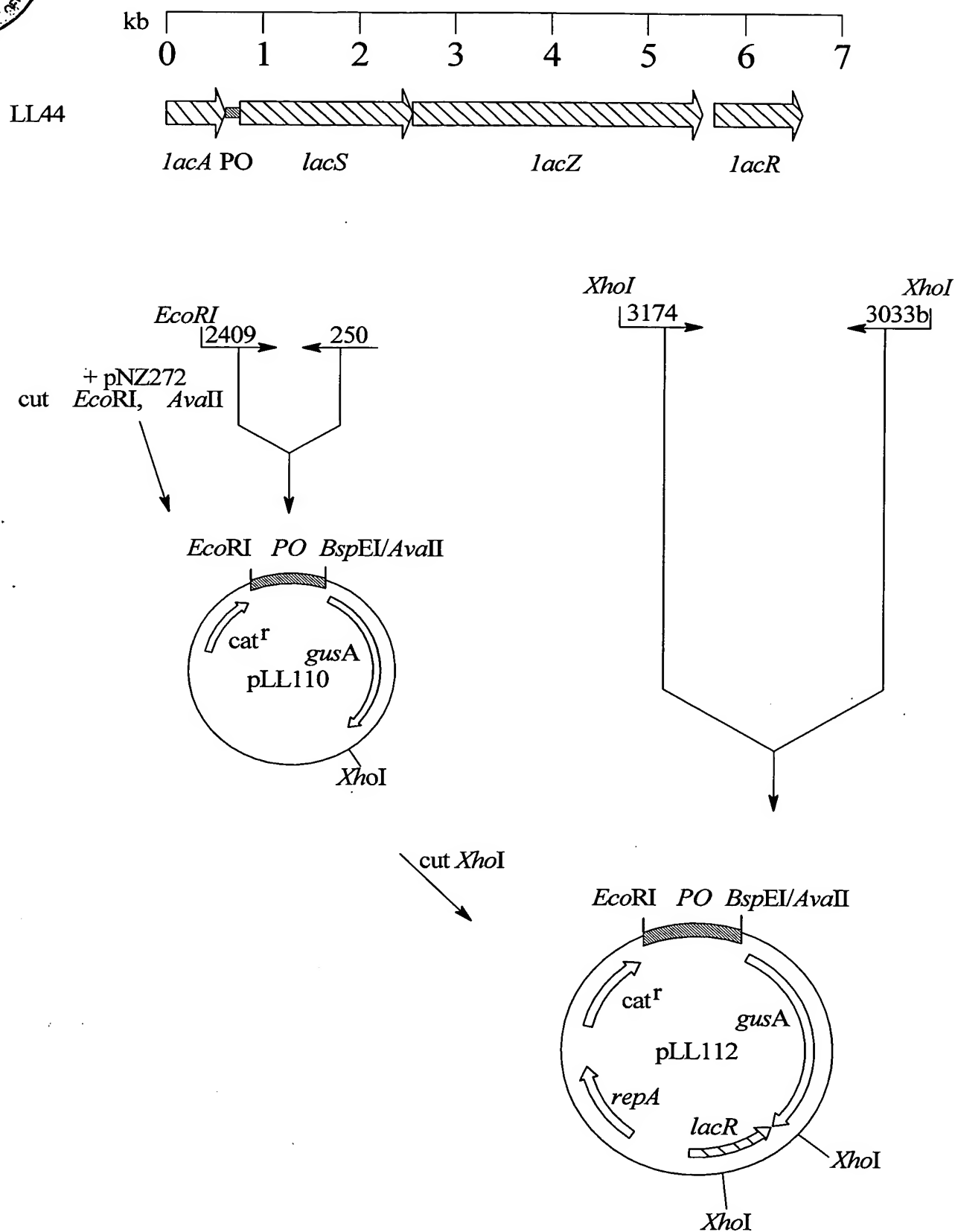


FIG. 7



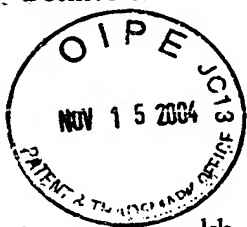


FIG. 8

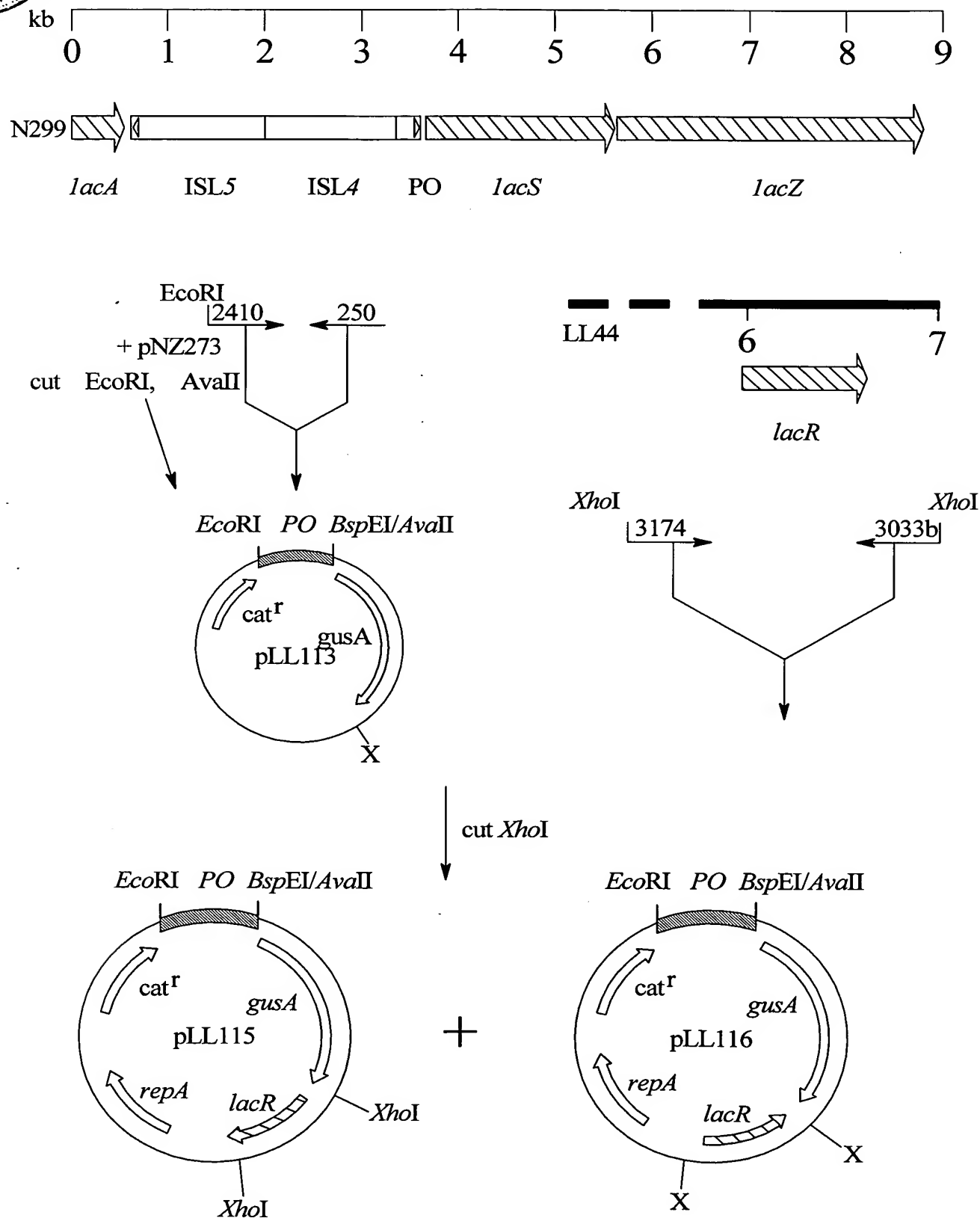
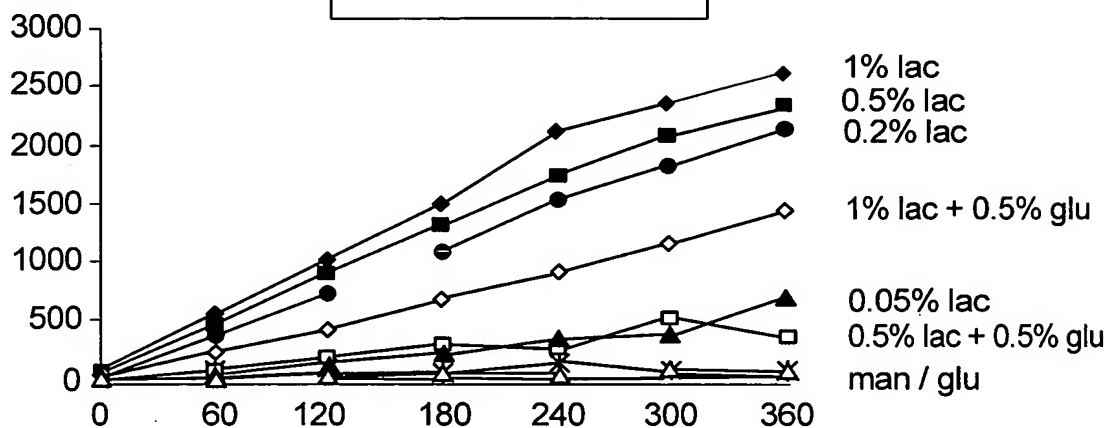


FIG. 9

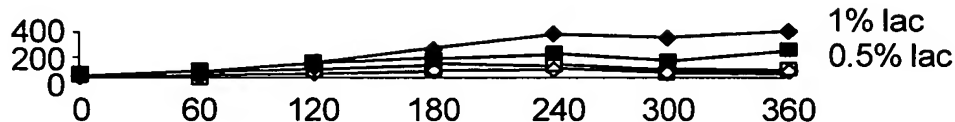
BEST AVAILABLE COPY

Bele-glucuronidase activity (Units/mg prot x 10⁻⁴)

pLL112
LL44 prom + *lacR* ←



pLL115
N299 prom + *lacR* →



pLL116
N299 prom + *lacR* ←

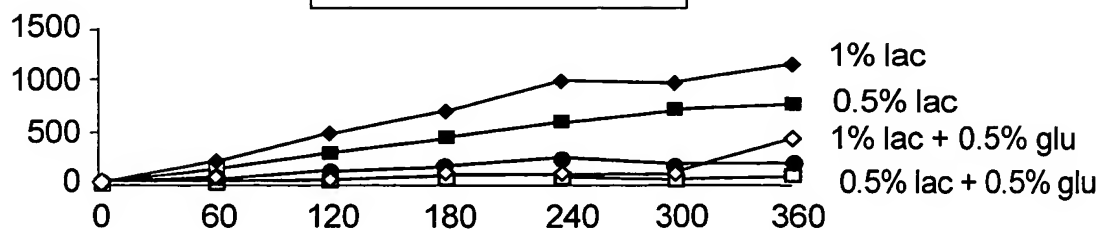
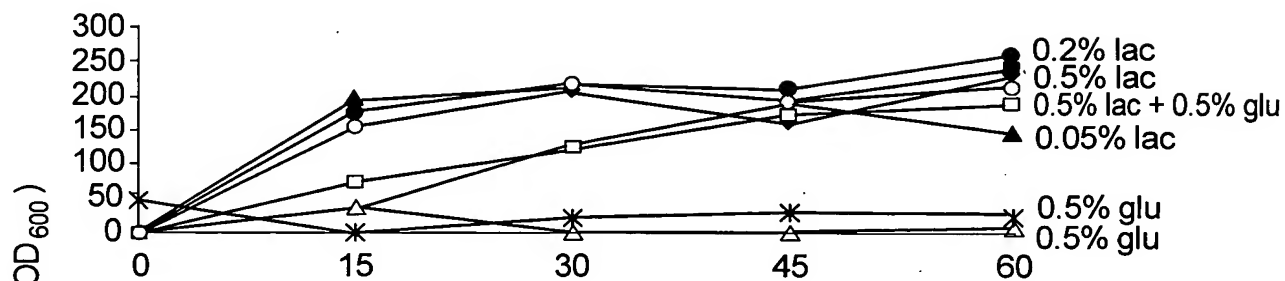




FIG. 10

LL44



N299

